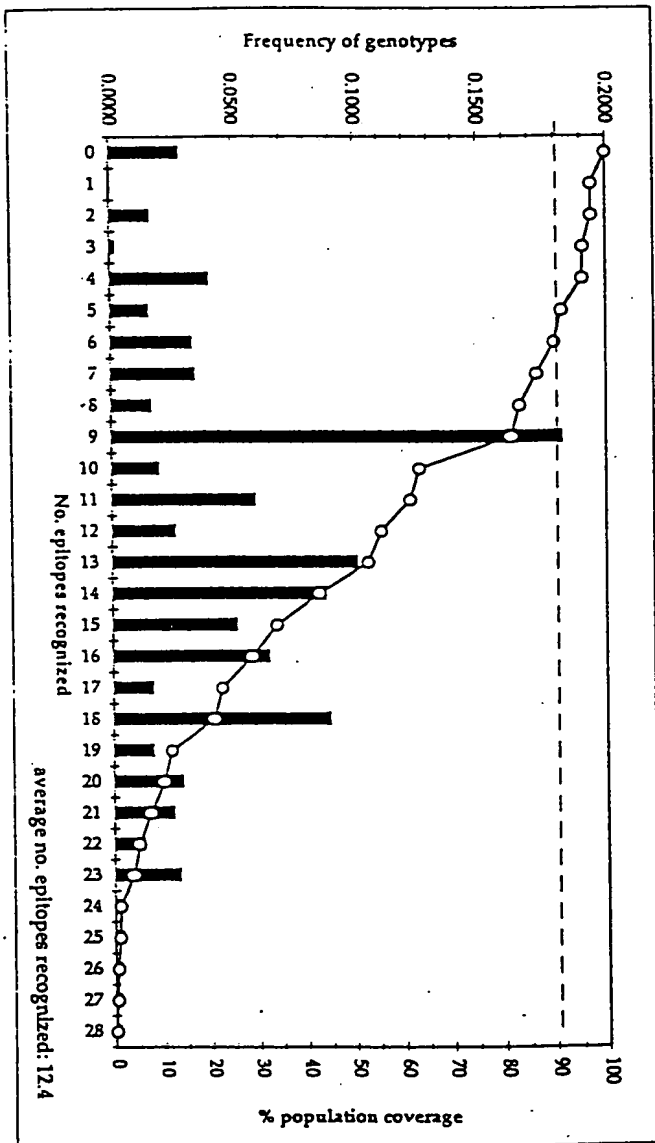


Figure 1. Monte Carlo population coverage analysis for
HBV candidate epitopes



Monte Carlo population coverage analysis for HBV candidate epitopes

Plot of total frequency of genotypes as a function of the number of HBV candidate epitopes bound by HLA-A and B alleles, in an average population. Genotype values were derived by averaging the gene frequencies in Caucasian, North American Black, Japanese, Chinese, and Hispanic populations. Also shown is the cumulative frequency of genotypes.

Using currently available HLA typing data, a residual fraction (about 15%) of the genes, in an average population, are unspecified. To arrive at 100% accounting of genes, a fraction of the residual has been added for each hlt population cluster in proportion to the relative frequency of the cluster within the HLA specified population.

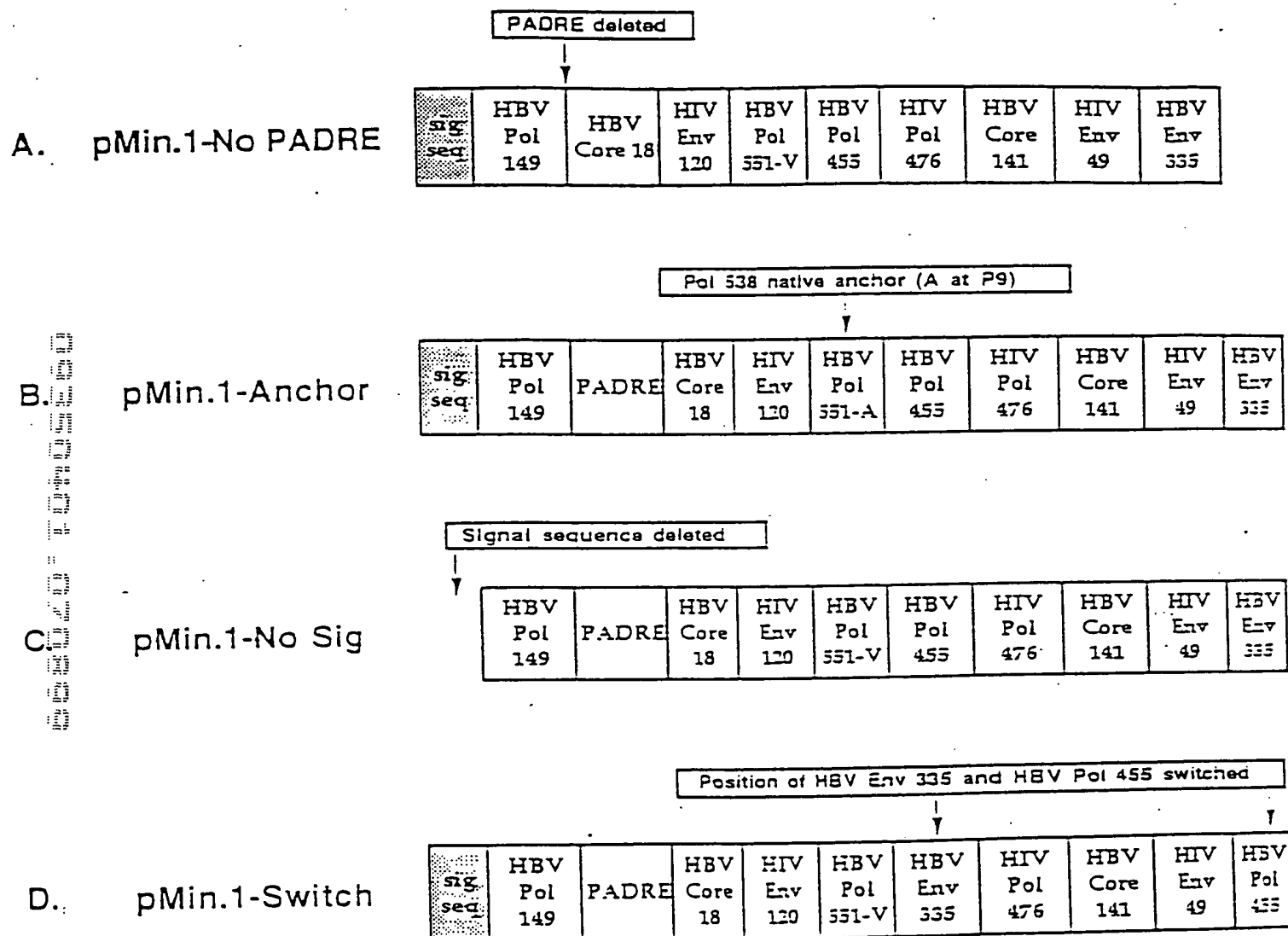


FIGURE 2